

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 25, 2005, 07:28:05 ; Search time 0.001 Seconds  
(without alignments)  
47.064 Million cell updates/sec

Title: US-09-997-641-387

Perfect score: 1102

Sequence: 1 MLWLFLFLVTAIHAEICQPG.....ENGIPSDPLDMKGILMPS 212

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 222 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : aab88580.genesep2001s.ig:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	97.4	222	1 aab88580	TOIG of: aab8858

ALIGNMENTS

RESULT 1  
aab88580  
TOIG of: aab88580 check: 7328 from: 1 to: 222

ID AAB88580 standard; protein; 222 AA.

AC AAB88580;

DT 04-JUN-2001 (first entry)

DE Human hydrophobic domain containing protein clone HP10720 #64.

KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;

KW antianaemic; vulnary; antitumor; osteoplastic; anti-inflammatory;

KW cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;

KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;

KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;

OS Homo sapiens.

PN WO200112660-A2.

PD 22-FEB-2001.

PF 10-AUG-2000; 2000WO-JP005356.

PR 17-AUG-1999; 99JP-00230344.  
PR 07-SEP-1999; 99JP-00252551.  
PR 01-OCT-1999; 99JP-00281132.  
PR 22-OCT-1999; 99JP-00301624.  
PR 04-NOV-1999; 99JP-00313877.

PA (SAGA) SAGAMI CHEM RES CENT.  
(PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI, 2001-160059/16.

DR N-PSDB; AAF94460.

PT Human proteins with hydrophobic domains and the DNAs which encode them  
are useful for treating autoimmune disorders, burns and tumors and for  
screening novel pharmaceuticals.

PS Claim 1; Page 354-355; 518pp; English.

CC AAF94417 to AAF94516 encode the human proteins given in AAB88557 to  
AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,  
anti-HIV, neuroprotective, antianaemic, vulnary, antitumor,  
osteoplastic, anti-inflammatory and cytostatic activities, and can be used  
in gene therapy. (I) can be used as pharmaceuticals and as antigens to  
prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes  
for genetic diagnosis and gene sources for gene therapy or for producing  
(I) in large quantities. Cells containing (I) are used for the detection  
of ligands or receptors corresponding to membrane or secretory proteins  
and to screen small molecule novel pharmaceuticals. Antibodies directed  
to (I) can be used for the detection, quantification and purification of  
(I). Activities of (I) may include cytokine and cell  
proliferation/differentiation function, immune stimulating or suppressing  
activity, haematopoiesis regulating activity, tissue growth activity,  
activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
and chromolytic activity, receptor/ligand activity and anti-inflammatory  
activity. (I) and (II) can be used to treat autoimmune disorders e.g.  
inflammatory bowel disease, HIV infections, anaemia, burns, ulcers, osteoporosis,  
inflammatory bowel disease and tumours. (I) and (II) can also be used for  
wound healing, as nutritional sources or supplements e.g. as amino acid,  
carbon or nitrogen source, to effect metabolism, catabolism, anabolism,  
processing and utilisation of dietary fat, protein, carbohydrate,  
vitamins and minerals, to effect behavioural characteristics, to affect  
appetite, and can act as antigens in vaccines to raise an immune response  
to the protein or another material cross-reactive with the protein

CC SQ Sequence 222 AA;

AB88580 Length: 222 August 24, 2005 15:14 Type: P Check: 7328 ..  
aab88580

Query Match 97.4%; Score 1073; DB 1; Length 222;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLFLFLVTAIHAEICQPGAENAFKVRISIRALDCKAYAMPTNEEYLFKAVAFSMRK 60

DB 1 MLWLFLFLVTAIHAEICQPGAENAFKVRISIRALDCKAYAMPTNEEYLFKAVAFSMRK 60

QY 61 VPRREATEISHVLLCVNTOQVSFWFVVTDSKNTLPAVEVQSAIMNKRIINNAFLND 120

DB 61 VPRREATEISHVLLCVNTOQVSFWFVVTDSKNTLPAVEVQSAIMNKRIINNAFLND 120

QY 121 QTEFLKIPSTLAPMPDPSVPIIIFGVFCIIIVAILLISGIWRRKKKPSSEVD 180

DB 121 QTEFLKIPSTLAPMPDPSVPIIIFGVFCIIIVAILLISGIWRRKKKPSSEVD 180

QY 181 DAEDKCNMTTENGIPSDPLDMKG 206

DB 181 DAEDKCNMTTENGIPSDPLDMKG 206

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Job time : 0.001 secs

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